

## **RAW SEQUENCE LISTING**

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Information Center (STIC) no errors detected.**

Application Serial Number: 10/542,178  
Source: PCT  
Date Processed by STIC: 07-21-05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 07/21/2005

PATENT APPLICATION: US/10/542,178

TIME: 09:41:32

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Output Set: N:\CRF4\07212005\J542178.raw

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3 <110> APPLICANT: University of Virginia Patent Foundation
4     Herr, John
5     Allis, C. David
6     Coonrad, Scott
7     Wang, Yanming
9 <120> TITLE OF INVENTION: ePAD, an Oocyte Specific Protein
11 <130> FILE REFERENCE: 00856-02
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/542,178
C--> 13 <141> CURRENT FILING DATE: 2005-07-08
13 <150> PRIOR APPLICATION NUMBER: 60/439,170
14 <151> PRIOR FILING DATE: 2003-01-10
16 <150> PRIOR APPLICATION NUMBER: 60/480,774
17 <151> PRIOR FILING DATE: 2003-06-19
19 <160> NUMBER OF SEQ ID NOS: 10
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 721
25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapiens
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35      20      25      30
38 Ile Cys Leu Asp Leu Ser Gly Cys Ala Pro Gln Lys Cys Gln Cys Phe
39      35      40      45
42 Thr Ile His Gly Ser Gly Arg Val Leu Ile Asp Val Ala Asn Thr Val
43      50      55      60
46 Ile Ser Glu Lys Glu Asp Ala Thr Ile Trp Trp Pro Leu Ser Asp Pro
47 65      70      75      80
50 Thr Tyr Ala Thr Val Lys Met Thr Ser Pro Ser Pro Ser Val Asp Ala
51      85      90      95
54 Asp Lys Val Ser Val Thr Tyr Tyr Gly Pro Asn Glu Asp Ala Pro Val
55      100     105     110
58 Gly Thr Ala Val Leu Tyr Leu Thr Gly Ile Glu Pro Phe Gly Ala Gln
59      115     120     125
62 Arg Ser Ser Ser Gln Ser Phe Val Pro Leu Leu Pro Val Ser Glu Val
63      130     135     140
66 Ser Gln Ala Gln Glu Ala Glu Val Ser Leu Glu Val Asp Ile Tyr Arg
67 145     150     155     160
70 Asn Gly Gln Val Glu Met Ser Ser Asp Lys Gln Ala Lys Lys Lys Trp
71      165     170     175
74 Ile Trp Gly Pro Ser Gly Trp Gly Ala Ile Leu Leu Val Asn Cys Asn

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75          180          185          190
78 Pro Ala Asp Val Gly Gln Gln Leu Glu Asp Lys Lys Thr Lys Lys Val
79          195          200          205
82 Ile Phe Ser Glu Glu Ile Thr Asn Leu Ser Gln Met Thr Leu Asn Val
83          210          215          220
86 Gln Gly Pro Ser Cys Ile Leu Lys Lys Tyr Arg Leu Val Leu His Thr
87 225          230          235          240
90 Ser Lys Glu Glu Ser Lys Lys Ala Arg Val Tyr Trp Pro Gln Lys Asp
91          245          250          255
94 Asn Ser Ser Thr Phe Glu Leu Val Leu Gly Pro Asp Gln His Ala Tyr
95          260          265          270
98 Thr Leu Ala Leu Leu Gly Asn His Leu Lys Glu Thr Phe Tyr Val Glu
99          275          280          285
102 Ala Ile Ala Phe Pro Ser Ala Glu Phe Ser Gly Leu Ile Ser Tyr Ser
103          290          295          300
106 Val Ser Leu Val Glu Glu Ser Gln Asp Pro Ser Ile Pro Glu Thr Val
107 305          310          315          320
110 Leu Tyr Lys Asp Thr Val Val Phe Arg Val Ala Pro Cys Val Phe Ile
111          325          330          335
114 Pro Cys Thr Gln Val Pro Leu Glu Val Tyr Leu Cys Arg Glu Leu Gln
115          340          345          350
118 Leu Gln Gly Phe Val Asp Thr Val Thr Lys Leu Ser Glu Lys Ser Asn
119          355          360          365
122 Ser Gln Val Ala Ser Val Tyr Glu Asp Pro Asn Arg Leu Gly Arg Trp
123          370          375          380
126 Leu Gln Asp Glu Met Ala Phe Cys Tyr Thr Gln Ala Pro His Lys Thr
127 385          390          395          400
130 Thr Ser Leu Ile Leu Asp Thr Pro Gln Ala Ala Asp Leu Asp Glu Phe
131          405          410          415
134 Pro Met Lys Tyr Ser Leu Ser Pro Gly Ile Gly Tyr Met Ile Gln Asp
135          420          425          430
138 Thr Glu Asp His Lys Val Ala Ser Met Asp Ser Ile Gly Asn Leu Met
139          435          440          445
142 Val Ser Pro Pro Val Lys Val Gln Gly Lys Glu Tyr Pro Leu Gly Arg
143          450          455          460
146 Val Leu Ile Gly Ser Ser Phe Tyr Pro Ser Ala Glu Gly Arg Ala Met
147 465          470          475          480
150 Ser Lys Thr Leu Arg Asp Phe Leu Tyr Ala Gln Gln Val Gln Ala Pro
151          485          490          495
154 Val Glu Leu Tyr Ser Asp Trp Leu Met Thr Gly His Val Asp Glu Phe
155          500          505          510
158 Met Cys Phe Ile Pro Thr Asp Asp Lys Asn Glu Gly Lys Lys Gly Phe
159          515          520          525
162 Leu Leu Leu Leu Ala Ser Pro Ser Ala Cys Tyr Lys Leu Phe Arg Glu
163          530          535          540
166 Lys Gln Lys Glu Gly Tyr Gly Asp Ala Leu Leu Phe Asp Glu Leu Arg
167 545          550          555          560
170 Ala Asp Gln Leu Leu Ser Asn Gly Arg Glu Ala Lys Thr Ile Asp Gln
171          565          570          575

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174 Leu Leu Ala Asp Glu Ser Leu Lys Lys Gln Asn Glu Tyr Val Glu Cys
175          580          585          590
178 Ile His Leu Asn Arg Asp Ile Leu Lys Thr Glu Leu Gly Leu Val Glu
179          595          600          605
182 Gln Asp Ile Ile Glu Ile Pro Gln Leu Phe Cys Leu Glu Lys Leu Thr
183          610          615          620
186 Asn Ile Pro Ser Asp Gln Gln Pro Lys Arg Ser Phe Ala Arg Pro Tyr
187 625          630          635          640
190 Phe Pro Asp Leu Leu Arg Met Ile Val Met Gly Lys Asn Leu Gly Ile
191          645          650          655
194 Pro Lys Pro Phe Gly Pro Gln Ile Lys Gly Thr Cys Cys Leu Glu Glu
195          660          665          670
198 Lys Ile Cys Cys Leu Leu Glu Pro Leu Gly Phe Lys Cys Thr Phe Ile
199          675          680          685
202 Asn Asp Phe Asp Cys Tyr Leu Thr Glu Val Gly Asp Ile Cys Ala Cys
203          690          695          700
206 Ala Asn Ile Arg Arg Val Pro Phe Ala Phe Lys Trp Trp Lys Met Val
207 705          710          715          720
210 Pro

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214 &lt;210&gt; SEQ ID NO: 2

215 &lt;211&gt; LENGTH: 2166

216 &lt;212&gt; TYPE: DNA

217 &lt;213&gt; ORGANISM: Homo sapiens

219 &lt;400&gt; SEQUENCE: 2

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222 agccctgtcc atgccgtttg tgtgttgggc acagaaatct gcttggatct cagcgggtgt      120
224 gccccccaga agtgccagtg cttcaccatc catggtctctg ggaggggtctt gatcgatgtg      180
226 gccaacacgg tgatttctga gaaggaggac gccaccatct ggtggccccct gtctgatccc      240
228 acgtacgcca cagtgaagat gacatcgccc agcccttcctg tggatgcgga taaggtctcg      300
230 gtcacatact atgggcccac cgaggatgcc cccgtgggca cagctgtgct gtacctcact      360
232 ggcattgaac cctttggagc tcagaggagc tcttctcagt cctttgtccc gctgcttcca      420
234 gtcagtgaag tgtctcaggc tcaggaggca gaggtctctc tagaggtaga catctaccgc      480
236 aatgggcaag ttgagatgtc aagtgacaaa caggctaaga aaaaatggat ctgggggtccc      540
238 agcggttggg gtgccatcct gcttgtgaat tgcaaccctg ctgatgtggg ccagcaactt      600
240 gaggacaaga aaaccaagaa agtgatcttt tcagaggaaa taacgaatct gtcccagatg      660
242 actctgaatg tccaaggccc cagctgtatc ttaaagaaat atcggctagt cctccatacc      720
244 tccaaggaag agtcgaagaa ggcgagagtc tactggcccc aaaaagacaa ctccagtacc      780
246 tttgagttgg tgctggggcc cgaccagcac gcctatacct tggccctcct cggggaaccac      840
248 ttgaaggaga ctttctacgt tgaagctata gcattcccat ctgccgaatt ctcaggcctc      900
250 atctcctact ctgtgtccct ggtggaggag tctcaagacc cgtcaattcc agagactgtg      960
252 ctgtacaaag acacggtggt gttccgggtg gctccctgtg tcttcattcc ctgtaccagg     1020
254 gtgcctctgg aggtttacct gtgcaggagg ctgcagctgc aggggtttgt ggacacagtg     1080
256 acgaagctga gtgagaagag caacagccag gtggcatctg tctatgagga cccaaccgc     1140
258 ctgggcaggt ggctccagga tgagatggcc ttctgttaca ccagggtccc ccacaagaca     1200
260 acgtccttga tctctgacac acctcaggcc gccgatctcg atgagttccc catgaagtac     1260
262 tcaactgagcc ctggtatttg ctacatgata caggacactg aggaccataa agtggccagc     1320
264 atggattcca ttgggaacct gatggtgtcc ccacctgtca aggtccaagg gaaagagtac     1380
266 ccgctgggca gagtctcat tggcagcagc ttttacccca gcgcagaggg ccgggccatg     1440
268 agtaagaccc tccgagactt cctctatgcc cagcaggtcc aagcgccggt ggagctctac     1500

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270 tcagattggc taatgactgg ccacgtggat gagttcatgt gcttcatccc cacagatgac 1560
272 aagaatgagg gcaaaaaggg ctctctgctg ctcttgccca gcccagtgct ctgctataaa 1620
274 ctgttccgag agaaacagaa ggaaggctat ggcgacgctc ttctgtttga tgagcttaga 1680
276 gcagatcagc tctgttctaa tggaaggga gcaaaaacca tcgaccaact tctggctgat 1740
278 gaaagcctga agaagcagaa tgaatacgtg gagtgcattc acctgaaccg tgacatcctg 1800
280 aagacggagc tgggcctggt ggaacaggac atcatcgaga ttccccagct gttctgcttg 1860
282 gagaagctga ctaacatccc ctctgaccag cagcccaaga ggtcctttgc gaggccatac 1920
284 ttccctgacc tggtgcggat gattgtgatg ggcaagaacc tggggatccc caagcctttt 1980
286 gggcccaaaa tcaaggggac ctgctgcctg gaagaaaaga tttgctgctt gctggagccc 2040
288 ctgggcttca agtgcacctt catcaatgac tttgactgtt acctgacaga ggtcggagac 2100
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307 20 25 30
310 Ile Ser Ser Ser Val Ile Ala Gly Lys Glu Asp Thr Val Val Trp Arg
311 35 40 45
314 Ser Met Asn His Pro Thr Val Ala Leu Val Arg Met Val Ala Pro Ser
315 50 55 60
318 Pro Thr Val Asp Glu Asp Lys Val Leu Val Ser Tyr Phe Cys Pro Asp
319 65 70 75 80
322 Gln Glu Val Pro Thr Ala Thr Ala Val Leu Phe Leu Thr Gly Ile Glu
323 85 90 95
326 Ile Ser Leu Glu Ala Asp Ile Tyr Arg Asp Gly Gln Leu Asp Met Pro
327 100 105 110
330 Ser Asp Lys Lys Ala Lys Lys Lys Trp Met Trp Gly Met Asn Gly Trp
331 115 120 125
334 Gly Ala Ile Leu Leu Val Asn Cys Ser Pro Asn Ala Val Gly Gln Pro
335 130 135 140
338 Asp Glu Gln Ser Phe Gln Glu Gly Pro Arg Glu Ile Gln Asn Asn Leu
339 145 150 155 160
342 Ser Gln Met Asn Val Thr Val Glu Gly Pro Thr Ser Ile Leu Gln Asn
343 165 170 175
346 Tyr Gln Leu Ile Leu His Thr Ser Glu Glu Glu Ala Lys Lys Thr Arg
347 180 185 190
350 Val Tyr Trp Ser Gln Arg Gly Ser Ser Ala Tyr Glu Leu Val Val Gly
351 195 200 205
354 Pro Asn Lys Pro Val Tyr Leu Leu Pro Thr Phe Glu Asn Arg Arg Lys
355 210 215 220
358 Glu Ala Phe Tyr Val Glu Ala Thr Glu Phe Pro Ser Pro Ser Phe Ser
359 225 230 235 240
362 Gly Leu Ile Ser Leu Ser Leu Ser Leu Val Glu Lys Ala His Asp Glu
363 245 250 255

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366 Cys Ile Pro Glu Ile Pro Leu Tyr Lys Asp Thr Val Met Phe Arg Val
367          260          265          270
370 Ala Pro Tyr Ile Phe Met Pro Ser Thr Gln Met Pro Leu Glu Val Tyr
371          275          280          285
374 Leu Cys Arg Glu Leu Gln Leu Gln Gly Phe Val Asp Ser Val Thr Lys
375          290          295          300
378 Leu Ser Glu Lys Ser Lys Val Gln Val Val Lys Val Tyr Glu Asp Pro
379 305          310          315          320
382 Asn Arg Gln Ser Lys Trp Leu Gln Asp Glu Met Ala Phe Cys Tyr Thr
383          325          330          335
386 Gln Ala Pro His Lys Thr Val Ser Leu Ile Leu Asp Thr Pro Arg Val
387          340          345          350
390 Ser Lys Leu Glu Asp Phe Pro Met Lys Tyr Thr Leu Thr Pro Gly Ser
391          355          360          365
394 Gly Tyr Leu Ile Arg Gln Ile Glu Asp His Arg Val Ala Ser Leu Asp
395          370          375          380
398 Ser Ile Gly Asn Leu Met Val Ser Pro Pro Val Lys Ala Gln Gly Lys
399 385          390          395          400
402 Asp Tyr Pro Leu Gly Arg Val Leu Ile Gly Gly Ser Phe Tyr Pro Ser
403          405          410          415
406 Ser Glu Gly Arg Asp Met Asn Lys Gly Leu Arg Glu Phe Val Tyr Ala
407          420          425          430
410 Gln Gln Val Gln Ala Pro Val Glu Leu Phe Ser Asp Trp Leu Met Thr
411          435          440          445
414 Gly His Met Asp Gln Phe Met Cys Phe Val Pro Thr Asn Asp Lys Asn
415          450          455          460
418 Asn Asp Gln Lys Asp Phe Arg Leu Leu Leu Ala Ser Pro Ser Ala Cys
419 465          470          475          480
422 Phe Glu Leu Phe Glu Gln Lys Gln Lys Glu Gly Tyr Gly Asn Val Thr
423          485          490          495
426 Leu Phe Glu Asp Ile Gly Ala Glu Gln Leu Leu Ser Asn Gly Arg Glu
427          500          505          510
430 Ser Lys Thr Ile Ser Gln Ile Leu Ala Asp Lys Ser Phe Arg Glu Gln
431          515          520          525
434 Asn Thr Tyr Val Glu Lys Cys Ile Ser Leu Asn Arg Thr Leu Leu Lys
435          530          535          540
438 Thr Glu Leu Gly Leu Glu Asp Lys Asp Ile Ile Leu Ile Pro Gln Leu
439 545          550          555          560
442 Phe Cys Leu Glu Gln Leu Thr Asn Val Pro Ser Asn Gln Gln Ser Thr
443          565          570          575
446 Lys Leu Phe Ala Arg Pro Tyr Phe Pro Asp Met Leu Gln Ile Ile Val
447          580          585          590
450 Leu Gly Lys Asn Leu Gly Ile Pro Lys Pro Phe Gly Pro Lys Ile Asn
451          595          600          605
454 Gly Thr Cys Cys Leu Glu Glu Lys Val Cys Gly Leu Leu Glu Pro Leu
455          610          615          620
458 Gly Leu Lys Cys Thr Phe Ile Asp Asp Phe Asp Cys Tyr Leu Ala Asn
459 625          630          635          640
462 Ile Gly Asp Val Cys Ala Ser Ala Ile Ile Asn Arg Val Pro Phe Ala

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/542,178

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date